

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (I) APPLICANT: Korenberg, Julie R.
- (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING DS-CAM
PROTEINS AND PRODUCTS RELATED THERETO
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Campbell and Flores
(B) STREET: 4370 La Jolla Village Drive, Suite 700
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92122
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/029,322
(B) FILING DATE: 25-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Ramos, Robert T.
(B) REGISTRATION NUMBER: 37,915
(C) REFERENCE/DOCKET NUMBER: P-CE 2817
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 619-535-9001
(B) TELEFAX: 619-535-8949

(2) INFORMATION FOR SEQ ID NO:1:

- (I) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6604 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 453..6185

0895591 102390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGACTGAGGC CGGAGCACGG CAAAGATGAG CCTGCCCGCC CGCCTGCTGC CTGGATGCGG	60
AGGGTGAGGG CTGGCGCACG GGAGGCCGCT GGCTGCGCAT TCTGGGCGCC GAGTGCCCGG	120
GATGAGCTCA CGCCCGCGTC TCGGGCTCTC TCCACCTGCC GACCTGCCGG GGGCCCACTG	180
AGCTGACGGC GCACCTGGGC TCCGGCCGCA GCGTGGGGCG CGGCGCCCGG GAGCAGGTGT	240
GCAGGAGCGC AGCGCGCGGC GAGCGCAGCC CTCGCTCCGG AGCCCGGCCG CGCCGCGTGC	300
CCGGGCGGCT AGGCAGCGGC GGCGGCGGCG GCGGGCGGCG GGCGGGCGGC GGCCCCCGGG	360
CAGGTGCCGA GCGGCGAGCG GAGCCGGGCC GGGCGGAGCG CGGGGGGCGA GGCCGGCGCG	420
TCGCTCGCGG GAGGCCGGGG AGCGGCAGGG GC ATG TGG ATA CTG GCT CTC TCC	473
Met Trp Ile Leu Ala Leu Ser	
1 5	
TTG TTC CAG AGC TTC GCG AAT GTT TTC AGT GAA GAC CTA CAC TCC AGC	521
Leu Phe Gln Ser Phe Ala Asn Val Phe Ser Glu Asp Leu His Ser Ser	
10 15 20	
CTC TAC TTT GTC AAT GCA TCT CTG CAA GAG GTA GTG TTT GCC AGC ACC	569
Leu Tyr Phe Val Asn Ala Ser Leu Gln Glu Val Val Phe Ala Ser Thr	
25 30 35	
ACG GGG ACT CTG GTG CCC TGC CCC GCA GCA GGC ATC CCT CCT GTG ACT	617
Thr Gly Thr Leu Val Pro Cys Pro Ala Ala Gly Ile Pro Pro Val Thr	
40 45 50 55	
CTC AGA TGG TAC CTA GCC ACG GGC GAG GAG ATC TAC GAT GTC CCC GGG	665
Leu Arg Trp Tyr Leu Ala Thr Gly Glu Glu Ile Tyr Asp Val Pro Gly	
60 65 70	
ATC CGC CAC GTC CAC CCC AAC GGC ACT CTC CAA ATT TTC CCC TTC CCT	713
Ile Arg His Val His Pro Asn Gly Thr Leu Gln Ile Phe Pro Phe Pro	
75 80 85	
CCT TCA AGC TTC AGT ACC TTA ATC CAT GAT AAT ACT TAT TAT TGC ACA	761
Pro Ser Ser Phe Ser Thr Leu Ile His Asp Asn Thr Tyr Tyr Cys Thr	
90 95 100	
GCT GAA AAT CCT TCA GGG AAA ATT AGA AGT CAG GAT GTC CAC ATC AAG	809
Ala Glu Asn Pro Ser Gly Lys Ile Arg Ser Gln Asp Val His Ile Lys	
105 110 115	
GCT GTT TTA CGG GAG CCC TAT ACA GTC CGT GTG GAG GAC CAG AAA ACC	857
Ala Val Leu Arg Glu Pro Tyr Thr Val Arg Val Glu Asp Gln Lys Thr	
120 125 130 135	
ATG AGA GGC AAT GTT GCG GTC TTC AAG TGC ATT ATC CCC TCC TCG GTG	905
Met Arg Gly Asn Val Ala Val Phe Lys Cys Ile Ile Pro Ser Ser Val	
140 145 150	
GAG GCG TAC ATC ACT GTC GTC TCA TGG GAG AAA GAC ACT GTT TCA CTT	953
Glu Ala Tyr Ile Thr Val Val Ser Trp Glu Lys Asp Thr Val Ser Leu	
155 160 165	
GTC TCA GGA TCT AGA TTT CTC ATC ACA TCC ACG GGA GCC TTG TAT ATT	1001
Val Ser Gly Ser Arg Phe Leu Ile Thr Ser Thr Gly Ala Leu Tyr Ile	
170 175 180	

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AAA Lys	GAT Asp	GTA Val	CAG Gln	AAT Asn	GAA Glu	GAT Asp	GGA Gly	TTG Leu	TAT Tyr	AAC Asn	TAC Tyr	CGC Arg	TGC Cys	ATC Ile	ACG Thr	1049
185						190					195					
CGG Arg	CAT His	CGA Arg	TAC Tyr	ACC Thr	GGA Gly	GAG Glu	ACG Thr	AGG Arg	CAG Gln	AGC Ser	AAC Asn	AGC Ser	GCC Ala	AGA Arg	CTT Leu	1097
200					205					210					215	
TTT Phe	GTA Val	TCA Ser	GAC Asp	CCA Pro	GCG Ala	AAC Asn	TCA Ser	GCC Ala	CCA Pro	TCC Ser	ATA Ile	CTG Leu	GAT Asp	GGG Gly	TTT Phe	1145
				220					225					230		
GAC Asp	CAT His	CGC Arg	AAA Lys	GCC Ala	ATG Met	GCT Ala	GGG Gly	CAG Gln	CGT Arg	GTG Val	GAG Glu	CTG Leu	CCT Pro	TGC Cys	AAA Lys	1193
			235					240					245			
GCG Ala	CTC Leu	GGG Gly	CAC His	CCT Pro	GAG Glu	CCA Pro	GAT Asp	TAC Tyr	CGC Arg	TGG Trp	CTG Leu	AAG Lys	GAC Asp	AAC Asn	ATG Met	1241
		250					255					260				
CCC Pro	CTG Leu	GAA Glu	CTT Leu	TCA Ser	GGG Gly	AGG Arg	TTC Phe	CAG Gln	AAG Lys	ACC Thr	GTG Val	ACG Thr	GGG Gly	CTG Leu	CTC Leu	1289
		265				270					275					
ATT Ile	GAG Glu	AAC Asn	ATT Ile	CGC Arg	CCC Pro	TCG Ser	GAC Asp	TCA Ser	GGC Gly	AGC Ser	TAT Tyr	GTT Val	TGT Cys	GAA Glu	GTG Val	1337
					285					290					295	
TCC Ser	AAC Asn	AGA Arg	TAC Tyr	GGA Gly	ACT Thr	GCT Ala	AAG Lys	GTG Val	ATA Ile	GGC Gly	CGC Arg	CTG Leu	TAC Tyr	GTG Val	AAA Lys	1385
				300					305					310		
CAG Gln	CCA Pro	CTG Leu	AAA Lys	GCC Ala	ACC Thr	ATC Ile	AGT Ser	CCC Pro	AGG Arg	AAG Lys	GTT Val	AAA Lys	AGC Ser	AGC Ser	GTG Val	1433
			315					320					325			
GGT Gly	AGC Ser	CAA Gln	GTT Val	TCC Ser	TTG Leu	TCC Ser	TGC Cys	AGC Ser	GTG Val	ACA Thr	GGA Gly	ACT Thr	GAG Glu	GAC Asp	CAG Gln	1481
		330					335					340				
GAA Glu	CTC Leu	TCC Ser	TGG Trp	TAC Tyr	CGC Arg	AAT Asn	GGT Gly	GAA Glu	ATC Ile	CTC Leu	AAC Asn	CCT Pro	GGA Gly	AAA Lys	AAT Asn	1529
		345				350					355					
GTG Val	AGG Arg	ATC Ile	ACA Thr	GGG Gly	ATC Ile	AAC Asn	CAC His	GAA Glu	AAC Asn	CTT Leu	ATA Ile	ATG Met	GAT Asp	CAC His	ATG Met	1577
					365					370					375	
GTC Val	AAA Lys	AGT Ser	GAC Asp	GGG Gly	GGC Gly	GCA Ala	TAC Tyr	CAG Gln	TGC Cys	TTT Phe	GTG Val	CGC Arg	AAG Lys	GAC Asp	AAG Lys	1625
				380					385					390		
CTG Leu	TCC Ser	GCT Ala	CAA Gln	GAC Asp	TAT Tyr	GTG Val	CAG Gln	GTG Val	GTC Val	CTT Leu	GAA Glu	GAT Asp	GGA Gly	ACT Thr	CCC Pro	1673
			395					400					405			
AAA Lys	ATT Ile	ATT Ile	TCT Ser	GCC Ala	TTT Phe	AGT Ser	GAA Glu	AAG Lys	GTG Val	GTG Val	AGT Ser	CCA Pro	GCA Ala	GAG Glu	CCG Pro	1721
			410				415					420				
GTT Val	TCC Ser	CTT Leu	ATG Met	TGC Cys	AAC Asn	GTG Val	AAG Lys	GGA Gly	ACA Thr	CCT Pro	TTG Leu	CCC Pro	ACG Thr	ATC Ile	ACG Thr	1769
		425				430					435					

TGG	ACC	CTG	GAC	GAT	GAC	CCG	ATT	CTC	AAG	GGT	GGC	AGT	CAC	CGC	ATC	1817
Trp	Thr	Leu	Asp	Asp	Asp	Pro	Ile	Leu	Lys	Gly	Gly	Ser	His	Arg	Ile	
440					445					450					455	
AGC	CAG	ATG	ATC	ACG	TCG	GAG	GGG	AAC	GTG	GTC	AGC	TAC	CTG	AAC	ATC	1865
Ser	Gln	Met	Ile	Thr	Ser	Glu	Gly	Asn	Val	Val	Ser	Tyr	Leu	Asn	Ile	
				460					465						470	
TCC	AGC	TCC	CAG	GTC	CGG	GAC	GGG	GGA	GTC	TAC	CGC	TGC	ACT	GCC	AAC	1913
Ser	Ser	Ser	Gln	Val	Arg	Asp	Gly	Gly	Val	Tyr	Arg	Cys	Thr	Ala	Asn	
			475					480					485			
AAC	TCG	GCG	GGA	GTC	GTC	CTG	TAC	CAG	GCT	CGA	ATA	AAC	GTA	AGA	GGG	1961
Asn	Ser	Ala	Gly	Val	Val	Leu	Tyr	Gln	Ala	Arg	Ile	Asn	Val	Arg	Gly	
		490					495					500				
CCT	GCA	AGC	ATT	CGA	CCA	ATG	AAA	AAC	ATC	ACA	GCA	ATA	GCA	GGA	CGG	2009
Pro	Ala	Ser	Ile	Arg	Pro	Met	Lys	Asn	Ile	Thr	Ala	Ile	Ala	Gly	Arg	
	505					510					515					
GAC	ACA	TAC	ATT	CAC	TGT	CGT	GTG	ATT	GGC	TAT	CCG	TAT	TAC	TCC	ATT	2057
Asp	Thr	Tyr	Ile	His	Cys	Arg	Val	Ile	Gly	Tyr	Pro	Tyr	Tyr	Ser	Ile	
520					525					530					535	
AAA	TGG	TAC	AAG	AAC	TCT	AAC	CTG	CTT	CCT	TTC	AAC	CAC	CGC	CAA	GTG	2105
Lys	Trp	Tyr	Lys	Asn	Ser	Asn	Leu	Leu	Pro	Phe	Asn	His	Arg	Gln	Val	
				540					545					550		
GCA	TTT	GAG	AAC	AAT	GGA	ACT	CTT	AAA	CTT	TCA	GAT	GTG	CAA	AAG	GAA	2153
Ala	Phe	Glu	Asn	Asn	Gly	Thr	Leu	Lys	Leu	Ser	Asp	Val	Gln	Lys	Glu	
			555					560					565			
GTG	GAC	GAG	GGG	GAG	TAC	ACG	TGC	AAC	GTG	TTG	GTT	CAA	CCA	CAA	CTC	2201
Val	Asp	Glu	Gly	Glu	Tyr	Thr	Cys	Asn	Val	Leu	Val	Gln	Pro	Gln	Leu	
	570						575					580				
TCC	ACC	AGC	CAG	AGC	GTC	CAC	GTG	ACC	GTG	AAA	GTT	CCG	CCT	TTC	ATA	2249
Ser	Thr	Ser	Gln	Ser	Val	His	Val	Thr	Val	Lys	Val	Pro	Pro	Phe	Ile	
	585					590					595					
CAA	CCC	TTT	GAG	TTT	CCA	AGA	TTC	TCC	ATT	GGG	CAG	CGG	GTC	TTC	ATC	2297
Gln	Pro	Phe	Glu	Phe	Pro	Arg	Phe	Ser	Ile	Gly	Gln	Arg	Val	Phe	Ile	
600					605					610					615	
CCC	TGT	GTT	GTG	GTC	TCA	GGG	GAC	TTA	CCC	ATC	ACG	ATC	ACC	TGG	CAG	2345
Pro	Cys	Val	Val	Val	Ser	Gly	Asp	Leu	Pro	Ile	Thr	Ile	Thr	Trp	Gln	
				620					625					630		
AAG	GAT	GGC	CGG	CCA	ATC	CCT	GGG	AGC	CTT	GGG	GTG	ACC	ATT	GAC	AAT	2393
Lys	Asp	Gly	Arg	Pro	Ile	Pro	Gly	Ser	Leu	Gly	Val	Thr	Ile	Asp	Asn	
			635					640					645			
ATT	GAC	TTC	ACG	AGC	TCC	TTG	AGG	ATT	TCC	AAT	CTC	TCG	CTC	ATG	CAC	2441
Ile	Asp	Phe	Thr	Ser	Ser	Leu	Arg	Ile	Ser	Asn	Leu	Ser	Leu	Met	His	
		650					655					660				
AAT	GGG	AAT	TAC	ACC	TGC	ATA	GCC	CGG	AAT	GAG	GCC	GCC	GCT	GTG	GAG	2489
Asn	Gly	Asn	Tyr	Thr	Cys	Ile	Ala	Arg	Asn	Glu	Ala	Ala	Ala	Val	Glu	
	665					670					675					
CAC	CAA	AGC	CAG	TTG	ATT	GTC	AGA	GTT	CCT	CCC	AAG	TTT	GTG	GTT	CAG	2537
His	Gln	Ser	Gln	Leu	Ile	Val	Arg	Val	Pro	Pro	Lys	Phe	Val	Val	Gln	
680					685					690					695	

CCT Pro	TCC Ser	TCC Ser	ACC Thr 955	TAC Tyr	AGC Ser	ATC Ile	CGC Arg	ATG Met 960	TAC Tyr	GCC Ala	AAG Lys	AAC Asn	CGG Arg 965	ATT Ile	GGC Gly	3353
AAG Lys	AGC Ser	GAG Glu 970	CCC Pro	AGC Ser	AAC Asn	GAG Glu	CTC Leu 975	ACC Thr	ATC Ile	ACG Thr	GCG Ala	GAC Asp 980	GAG Glu	GCA Ala	GCT Ala	3401
CCT Pro	GAT Asp 985	GGT Gly	CCA Pro	CCT Pro	CAG Gln	GAA Glu 990	GTT Val	CAC His	CTG Leu	GAG Glu	CCT Pro 995	ATA Ile	TCA Ser	TCT Ser	CAG Gln	3449
AGC Ser 1000	ATC Ile	AGG Arg	GTC Val	ACA Thr	TGG Trp 1005	AAG Lys	GCT Ala	CCC Pro	AAG Lys	AAA Lys 1010	CAT His	TTG Leu	CAA Gln	AAT Asn	GGG Gly 1015	3497
ATT Ile	ATC Ile	CGT Arg	GGC Gly	TAC Tyr 1020	CAA Gln	ATA Ile	GGT Gly	TAC Tyr	CGA Arg 1025	GAG Glu	TAC Tyr	AGC Ser	ACT Thr	GGG Gly 1030	GGT Gly	3545
AAC Asn	TTC Phe	CAA Gln 1035	TTC Phe	AAC Asn	ATT Ile	ATC Ile	AGT Ser 1040	GTC Val	GAC Asp	ACC Thr	AGC Ser	GGG Gly 1045	GAC Asp	AGT Ser	GAG Glu	3593
GTT Val	TAC Tyr 1050	ACC Thr	CTG Leu	GAC Asp	AAC Asn	CTG Leu	AAT Asn 1055	AAG Lys	TTC Phe	ACT Thr	CAG Gln 1060	TAC Tyr	GGC Gly	CTG Leu	GTG Val	3641
GTG Val 1065	CAG Gln 1065	GCC Ala	TGT Cys	AAC Asn	CGG Arg	GCC Ala 1070	GGC Gly	ACG Thr	GGG Gly	CCT Pro	TCT Ser 1075	TCT Ser	CAG Gln	GAA Glu	ATC Ile	3689
ATC Ile 1080	ACC Thr	ACC Thr	ACT Thr	CTC Leu	GAG Glu 1085	GAT Asp	GTG Val	CCC Pro	AGT Ser	TAC Tyr 1090	CCC Pro	CCC Pro	GAA Glu	AAT Asn	GTC Val 1095	3737
CAA Gln	GCC Ala	ATA Ile	GCA Ala 1100	ACA Thr	TCA Ser	CCA Pro	GAA Glu	AGC Ser	ATA Ile 1105	TCA Ser	ATA Ile	TCC Ser	TGG Trp	TCC Ser 1110	ACA Thr	3785
CTT Leu	TCC Ser	AAG Lys	GAA Glu 1115	GCC Ala	TTG Leu	AAT Asn	GGA Gly	ATT Ile 1120	CTC Leu	CAG Gln	GGG Gly	TTC Phe	AGA Arg 1125	GTC Val	ATT Ile	3833
TAC Tyr	TGG Trp 1130	GCC Ala	AAC Asn	CTC Leu	ATG Met	GAC Asp	GGA Gly 1135	GAG Glu	CTG Leu	GGT Gly	GAG Glu	ATT Ile 1140	AAA Lys	AAC Asn	ATC Ile	3881
ACC Thr	ACC Thr 1145	ACA Thr	CAG Gln	CCT Pro	TCA Ser	CTG Leu 1150	GAG Glu	CTG Leu	GAC Asp	GGG Gly	CTG Leu 1155	GAA Glu	AAG Lys	TAC Tyr	ACC Thr	3929
AAC Asn 1160	TAC Tyr	AGC Ser	ATC Ile	CAG Gln	GTG Val 1165	CTG Leu	GCC Ala	TTC Phe	ACC Thr	CGC Arg 1170	GCA Ala	GGA Gly	GAC Asp	GGG Gly	GTC Val 1175	3977
AGG Arg	AGT Ser	GAG Glu	CAG Gln	ATC Ile 1180	TTC Phe	ACC Thr	CGG Arg	ACC Thr	AAA Lys 1185	GAG Glu	GAT Asp	GTT Val	CCA Pro	GGT Gly 1190	CCT Pro	4025
CCC Pro	GCG Ala	GGT Gly	GTG Val 1195	AAG Lys	GCA Ala	GCG Ala	GCG Ala	GCC Ala 1200	TCA Ser	GCC Ala	TCC Ser	ATG Met	GTC Val 1205	TTT Phe	GTG Val	4073

TCC Ser	TGG Trp	CTT Leu 1210	CCC Pro	CCT Pro	CTC Leu	AAG Lys	CTG Leu 1215	AAC Asn	GGC Gly	ATC Ile	ATC Ile	CGA Arg 1220	AAG Lys	TAC Tyr	ACT Thr	4121
GTA Val	TTC Phe 1225	TGC Cys	TCC Ser	CAC His	CCC Pro	TAT Tyr 1230	CCC Pro	ACA Thr	GTG Val	ATC Ile	AGC Ser 1235	GAG Glu	TTT Phe	GAG Glu	GCC Ala	4169
TCT Ser 1240	CCC Pro	GAC Asp	TCG Ser	TTT Phe	TCC Ser 1245	TAC Tyr	AGA Arg	ATT Ile	CCC Pro	AAC Asn 1250	CTG Leu	AGT Ser	AGG Arg	AAT Asn	CGT Arg 1255	4217
CAG Gln	TAC Tyr	AGC Ser	GTC Val	TGG Trp 1260	GTG Val	GTG Val	GCT Ala	GTT Val	ACT Thr 1265	TCA Ser	GCC Ala	GGA Gly	AGA Arg	GGC Gly 1270	AAC Asn	4265
AGC Ser	AGT Ser	GAA Glu 1275	ATC Ile	ATC Ile	ACA Thr	GTC Val	GAG Glu	CCA Pro 1280	CTA Leu	GCA Ala	AAA Lys	GCT Ala	CCT Pro 1285	GCA Ala	CGA Arg	4313
ATC Ile	CTG Leu 1290	ACC Thr	TTC Phe	AGT Ser	GGG Gly	ACA Thr	GTG Val 1295	ACT Thr	ACT Thr	CCA Pro	TGG Trp	ATG Met 1300	AAA Lys	GAC Asp	ATT Ile	4361
GTC Val 1305	TTG Leu	CCT Pro	TGT Cys	AAG Lys	GCT Ala	GTT Val 1310	GGG Gly	GAC Asp	CCT Pro	TCT Ser	CCT Pro 1315	GCA Ala	GTC Val	AAA Lys	TGG Trp	4409
ATG Met 1320	AAA Lys	GAC Asp	AGT Ser	AAC Asn	GGG Gly 1325	ACA Thr	CCC Pro	AGT Ser	CTA Leu	GTA Val 1330	ACG Thr	ATT Ile	GAT Asp	GGG Gly	CGG Arg 1335	4457
AGG Arg	AGC Ser	ATC Ile	TTT Phe	AGC Ser 1340	AAC Asn	GGA Gly	AGC Ser	TTC Phe 1345	ATT Ile	ATT Ile	CGC Arg	ACG Thr	GTG Val	AAA Lys 1350	GCA Ala	4505
GAA Glu	GAC Asp	TCC Ser	GGC Gly 1355	TAT Tyr	TAC Tyr	AGC Ser	TGC Cys	ATT Ile 1360	GCC Ala	AAT Asn	AAC Asn	AAC Asn	TGG Trp 1365	GGA Gly	TCT Ser	4553
GAT Asp	GAA Glu 1370	ATT Ile	ATT Ile	TTA Leu	AAC Asn	TTA Leu	CAA Gln 1375	GTA Val	CAA Gln	GTT Val	CCA Pro 1380	CCA Pro	GAT Asp	CAG Gln	CCT Pro	4601
CGG Arg 1385	CTT Leu	ACA Thr	GTC Val	TCC Ser	AAG Lys	ACC Thr 1390	ACG Thr	TCT Ser	TCC Ser	TCC Ser	ATC Ile 1395	ACC Thr	CTT Leu	TCT Ser	TGG Trp	4649
CTC Leu 1400	CCT Pro	GGA Gly	GAC Asp	AAC Asn	GGG Gly 1405	GGC Gly	AGC Ser	TCT Ser	ATC Ile	AGA Arg 1410	GGA Gly	TAC Tyr	ATA Ile	CTG Leu	CAG Gln 1415	4697
TAC Tyr	TCC Ser	GAG Glu	GAC Asp	AAT Asn 1420	AGT Ser	GAG Glu	CAG Gln	TGG Trp	GGG Gly 1425	AGT Ser	TTT Phe	CCA Pro	ATC Ile	AGC Ser 1430	CCC Pro	4745
AGC Ser	GAA Glu	CGT Arg	TCC Ser 1435	TAT Tyr	CGC Arg	TTG Leu	GAA Glu	AAT Asn 1440	CTC Leu	AAA Lys	TGT Cys	GGG Gly	ACT Thr 1445	TGG Trp	TAT Tyr	4793
AAG Lys	TTC Phe 1450	ACA Thr	CTG Leu	ACA Thr	GCC Ala	CAA Gln 1455	AAT Asn	GGA Gly	GTG Val	GGC Gly	CCA Pro	GGG Gly 1460	CGC Arg	ATA Ile	AGT Ser	4841

GAA ATC ATA GAA GCA AAG ACC TTA GGA AAA GAG CCC CAG TTC TCA AAG Glu Ile Ile Glu Ala Lys Thr Leu Gly Lys Glu Pro Gln Phe Ser Lys 1465 1470 1475	4889
GAG CAG GAG CTG TTT GCC AGC ATC AAC ACC ACA CGC GTG AGG CTG AAC Glu Gln Glu Leu Phe Ala Ser Ile Asn Thr Thr Arg Val Arg Leu Asn 1480 1485 1490 1495	4937
CTC ATT GGC TGG AAT GAT GGC GGC TGC CCC ATC ACC TCC TTC ACA CTA Leu Ile Gly Trp Asn Asp Gly Gly Cys Pro Ile Thr Ser Phe Thr Leu 1500 1505 1510	4985
GAG TAC AGG CCC TTT GGG ACC ACA GTT TGG ACC ACA GCT CAG AGG ACC Glu Tyr Arg Pro Phe Gly Thr Thr Val Trp Thr Thr Ala Gln Arg Thr 1515 1520 1525	5033
TCT CTC TCC AAG TCC TAC ATC CTG TAT GAC CTG CAG GAA GCC ACC TGG Ser Leu Ser Lys Ser Tyr Ile Leu Tyr Asp Leu Gln Glu Ala Thr Trp 1530 1535 1540	5081
TAT GAG CTG CAG ATG CGG GTG TGC AAC AGT GCG GGC TGC GCG GAG AAG Tyr Glu Leu Gln Met Arg Val Cys Asn Ser Ala Gly Cys Ala Glu Lys 1545 1550 1555	5129
CAG GCC AAC TTC GCT ACG CTG AAC TAC GAT GGC AGT ACA ATT CCT CCA Gln Ala Asn Phe Ala Thr Leu Asn Tyr Asp Gly Ser Thr Ile Pro 1560 1565 1570 1575	5177
CTC ATT AAG TCA GTT GTC CAA AAC GAA GAA GGG CTG ACG ACC AAC GAG Leu Ile Lys Ser Val Val Gln Asn Glu Glu Gly Leu Thr Thr Asn Glu 1580 1585 1590	5225
GGG CTC AAG ATG CTG GTG ACC ATC TCC TGT ATC CTG GTG GGG GTC TTG Gly Leu Lys Met Leu Val Thr Ile Ser Cys Ile Leu Val Gly Val Leu 1595 1600 1605	5273
CTG CTG TTT GTG CTC CTG CTG GTT GTG CGG AGG AGG CGG CGG GAG CAG Leu Leu Phe Val Leu Leu Leu Val Val Arg Arg Arg Arg Glu Gln 1610 1615 1620	5321
AGG CTA AAG AGG CTG CGA GAT GCA AAG AGT TTA GCT GAA ATG CTC ATG Arg Leu Lys Arg Leu Arg Asp Ala Lys Ser Leu Ala Glu Met Leu Met 1625 1630 1635	5369
AGT AAG AAT ACC CGG ACT TCA GAT ACG TTA AGC AAG CAA CAG CAG ACC Ser Lys Asn Thr Arg Thr Ser Asp Thr Leu Ser Lys Gln Gln Gln Thr 1640 1645 1650 1655	5417
CTG CGA ATG CAC ATC GAC ATA CCC AGG GCT CAG CTT TTG ATT GAA GAG Leu Arg Met His Ile Asp Ile Pro Arg Ala Gln Leu Leu Ile Glu Glu 1660 1665 1670	5465
AGA GAC ACG ATG GAG ACC ATT GAT GAT CGC TCC ACG GTT CTG TTG ACG Arg Asp Thr Met Glu Thr Ile Asp Asp Arg Ser Thr Val Leu Leu Thr 1675 1680 1685	5513
GAT GCT GAC TTT GGA GAG GCA GCT AAG CAG AAG TCC CTG ACG GTC ACT Asp Ala Asp Phe Gly Glu Ala Ala Lys Gln Lys Ser Leu Thr Val Thr 1690 1695 1700	5561
CAC ACG GTC CAT TAC CAA TCG GTG TCT CAG GCC ACT GGG CCC TTA GTG His Thr Val His Tyr Gln Ser Val Ser Gln Ala Thr Gly Pro Leu Val 1705 1710 1715	5609

GAT GTT TCA GAC GCT CGG CCG GGA ACG AAT CCC ACC ACC AGG AGG AAT Asp Val Ser Asp Ala Arg Pro Gly Thr Asn Pro Thr Thr Arg Arg Asn 1720 1725 1730 1735	5657
GCC AAG GCT GGG CCC ACA GCG AGA AAC CGC TAT GCC AGC CAG TGG ACC Ala Lys Ala Gly Pro Thr Ala Arg Asn Arg Tyr Ala Ser Gln Trp Thr 1740 1745 1750	5705
CTC AAC CGA CCC CAC CCC ACC ATC TCA GCA CAC ACC CTC ACC ACA GAC Leu Asn Arg Pro His Pro Thr Ile Ser Ala His Thr Leu Thr Thr Asp 1755 1760 1765	5753
TGG AGG CTG CCA ACA CCC AGG GCT GCA GGA TCA GTA GAC AAA GAG AGC Trp Arg Leu Pro Thr Pro Arg Ala Ala Gly Ser Val Asp Lys Glu Ser 1770 1775 1780	5801
GAC AGT TAC AGC GTC AGC CCC TCG CAA GAC ACA GAT CGA GCA AGA AGC Asp Ser Tyr Ser Val Ser Pro Ser Gln Asp Thr Asp Arg Ala Arg Ser 1785 1790 1795	5849
AGC ATG GTC TCC ACA GAA AGT GCC TCC TCC ACT TAC GAA GAA CTG GCC Ser Met Val Ser Thr Glu Ser Ala Ser Ser Thr Tyr Glu Glu Leu Ala 1800 1805 1810 1815	5897
AGG GCC TAC GAA CAC GCC AAG ATG GAA GAG CAA CTG AGG CAC GCC AAG Arg Ala Tyr Glu His Ala Lys Met Glu Glu Gln Leu Arg His Ala Lys 1820 1825 1830	5945
TTC ACC ATC ACG GAG TGC TTC ATA TCA GAC ACG TCA TCG GAG CAG TTG Phe Thr Ile Thr Glu Cys Phe Ile Ser Asp Thr Ser Ser Glu Gln Leu 1835 1840 1845	5993
ACG GCA GGG ACA AAT GAG TAC ACG GAC AGT CTG ACC TCC AGC ACC CCT Thr Ala Gly Thr Asn Glu Tyr Thr Asp Ser Leu Thr Ser Ser Thr Pro 1850 1855 1860	6041
TCC GAA TCG GGA ATC TGC AGG TTC ACT GCA TCT CCC CCC AAA CCT CAG Ser Glu Ser Gly Ile Cys Arg Phe Thr Ala Ser Pro Pro Lys Pro Gln 1865 1870 1875	6089
GAT GGA GGA AGA GTA ATG AAT ATG GCA GTT CCA AAG GCA ATC GGC CAG Asp Gly Gly Arg Val Met Asn Met Ala Val Pro Lys Ala Ile Gly Gln 1880 1885 1890 1895	6137
GTG ACC TCA TAC ATT TGC CTC CAT ACC TTA GAA TGG ACT TTT TGT TAAACCGAGG Val Thr Ser Tyr Ile Cys Leu His Thr Leu Glu Trp Thr Phe Cys 1900 1905 1910	
TGGTCCAGGC ACCAGCAGGG ACCTGAGCTT AGGACAAGCA TGCTTGGAAC CTCAGAAAAG	6252
CCGGACCCTG AAGCGCCCCA CGGTCCTGGA GCCCATCCCG ATGGAAGCCG CCTCCTCCGC	6312
CTCCTCCACG AGAGAAGGAC AGTCGTGGCA GCCGGGGGCC GTGGCCACAT TACCTCAGCG	6372
GGAGGGAGCA GAGCTGGGAC AGGCAGCTAA AATGAGCAGC TCCCAAGAAT CACTGCTCGA	6432
CTCCCGGGGC CATTTGAAAG GAAACAATCC TTACGCAAAA TCTTACACCC TGGTATAACA	6492
GACAGCATGA CTGGACAGCG GTTGTAATA CAATTCAAAC AATTCAATCA AAGCTACCTT	6552
TTTTTTACGG AATTCCAATA TTTATAATTA AAGAAAATTG CCAAAATATA TT	6604

0095694 10229

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1910 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met 1	Trp	Ile	Leu	Ala 5	Leu	Ser	Leu	Phe	Gln 10	Ser	Phe	Ala	Asn	Val 15	Phe
Ser	Glu	Asp	Leu 20	His	Ser	Ser	Leu	Tyr 25	Phe	Val	Asn	Ala	Ser 30	Leu	Gln
Glu	Val	Val 35	Phe	Ala	Ser	Thr	Thr 40	Gly	Thr	Leu	Val	Pro 45	Cys	Pro	Ala
Ala	Gly 50	Ile	Pro	Pro	Val	Thr 55	Leu	Arg	Trp	Tyr	Leu 60	Ala	Thr	Gly	Glu
Glu 65	Ile	Tyr	Asp	Val	Pro 70	Gly	Ile	Arg	His	Val 75	His	Pro	Asn	Gly	Thr 80
Leu	Gln	Ile	Phe	Pro 85	Phe	Pro	Pro	Ser	Ser 90	Phe	Ser	Thr	Leu	Ile 95	His
Asp	Asn	Thr	Tyr 100	Tyr	Cys	Thr	Ala	Glu 105	Asn	Pro	Ser	Gly	Lys 110	Ile	Arg
Ser	Gln	Asp 115	Val	His	Ile	Lys	Ala 120	Val	Leu	Arg	Glu	Pro 125	Tyr	Thr	Val
Arg	Val 130	Glu	Asp	Gln	Lys	Thr 135	Met	Arg	Gly	Asn	Val 140	Ala	Val	Phe	Lys
Cys 145	Ile	Ile	Pro	Ser	Ser 150	Val	Glu	Ala	Tyr	Ile 155	Thr	Val	Val	Ser	Trp 160
Glu	Lys	Asp	Thr	Val 165	Ser	Leu	Val	Ser	Gly 170	Ser	Arg	Phe	Leu	Ile 175	Thr
Ser	Thr	Gly	Ala 180	Leu	Tyr	Ile	Lys	Asp 185	Val	Gln	Asn	Glu	Asp 190	Gly	Leu
Tyr	Asn	Tyr 195	Arg	Cys	Ile	Thr	Arg 200	His	Arg	Tyr	Thr	Gly 205	Glu	Thr	Arg
Gln	Ser 210	Asn	Ser	Ala	Arg	Leu 215	Phe	Val	Ser	Asp	Pro 220	Ala	Asn	Ser	Ala
Pro 225	Ser	Ile	Leu	Asp	Gly 230	Phe	Asp	His	Arg	Lys 235	Ala	Met	Ala	Gly	Gln 240
Arg	Val	Glu	Leu	Pro 245	Cys	Lys	Ala	Leu	Gly 250	His	Pro	Glu	Pro	Asp 255	Tyr
Arg	Trp	Leu	Lys 260	Asp	Asn	Met	Pro	Leu 265	Glu	Leu	Ser	Gly	Arg 270	Phe	Gln

Ile 610	Gly 610	Gln 610	Arg 610	Val 610	Phe 610	Ile 615	Pro 615	Cys 615	Val 615	Val 620	Ser 620	Gly 620	Asp 620	Leu 620
Pro 625	Ile 625	Thr 625	Ile 625	Thr 625	Trp 630	Gln 630	Lys 630	Asp 630	Gly 630	Arg 635	Pro 635	Ile 635	Pro 635	Ser 640
Leu 645	Gly 645	Val 645	Thr 645	Ile 645	Asp 645	Asn 645	Ile 645	Asp 645	Phe 650	Thr 650	Ser 650	Ser 650	Leu 655	Ile 655
Ser 660	Asn 660	Leu 660	Ser 660	Leu 660	Met 660	His 660	Asn 660	Gly 665	Asn 665	Tyr 665	Thr 665	Cys 665	Ile 670	Ala 670
Asn 675	Glu 675	Ala 675	Ala 675	Ala 675	Val 675	Glu 680	His 680	Gln 680	Ser 680	Gln 680	Leu 680	Ile 685	Val 685	Arg 685
Pro 690	Pro 690	Lys 690	Phe 690	Val 690	Val 690	Gln 695	Pro 695	Arg 695	Asp 695	Gln 695	Asp 700	Gly 700	Ile 700	Tyr 700
Lys 705	Ala 705	Val 705	Ile 705	Leu 705	Asn 710	Cys 710	Ser 710	Ala 710	Glu 710	Gly 715	Tyr 715	Pro 715	Val 715	Thr 720
Ile 725	Val 725	Trp 725	Lys 725	Phe 725	Ser 725	Lys 725	Gly 725	Ala 725	Gly 730	Val 730	Pro 730	Gln 730	Phe 735	Pro 735
Ile 740	Ala 740	Leu 740	Asn 740	Gly 740	Arg 740	Ile 740	Gln 740	Val 745	Leu 745	Ser 745	Asn 745	Gly 745	Ser 750	Leu 750
Ile 755	Lys 755	His 755	Val 755	Val 755	Glu 755	Glu 755	Asp 760	Ser 760	Gly 760	Tyr 760	Tyr 760	Leu 765	Cys 765	Val 765
Ser 770	Asn 770	Asp 770	Val 770	Gly 770	Ala 770	Asp 775	Val 775	Ser 775	Lys 775	Ser 775	Met 780	Tyr 780	Leu 780	Val 780
Lys 785	Ile 785	Pro 785	Ala 785	Met 785	Ile 790	Thr 790	Ser 790	Tyr 790	Pro 790	Asn 795	Thr 795	Thr 795	Leu 800	Thr 800
Gln 805	Gly 805	Gln 805	Lys 805	Lys 805	Glu 805	Met 805	Ser 805	Cys 805	Thr 810	Ala 810	His 810	Gly 810	Glu 815	Pro 815
Ile 820	Ile 820	Val 820	Arg 820	Trp 820	Glu 820	Lys 820	Glu 820	Asp 825	Arg 825	Ile 825	Ile 825	Asn 830	Pro 830	Met 830
Ala 835	Arg 835	Tyr 835	Leu 835	Val 835	Ser 835	Thr 835	Lys 840	Glu 840	Val 840	Gly 840	Glu 845	Glu 845	Val 845	Ser 845
Thr 850	Leu 850	Gln 850	Ile 850	Leu 850	Pro 850	Thr 855	Val 855	Arg 855	Glu 855	Asp 855	Ser 860	Gly 860	Phe 860	Ser 860
Cys 865	His 865	Ala 865	Ile 865	Asn 865	Ser 870	Tyr 870	Gly 870	Glu 870	Asp 875	Arg 875	Gly 875	Ile 875	Ile 875	Leu 880
Thr 885	Val 885	Gln 885	Glu 885	Pro 885	Pro 885	Asp 885	Pro 885	Pro 885	Glu 890	Ile 890	Glu 890	Ile 890	Lys 895	Val 895
Lys 900	Ala 900	Arg 900	Thr 900	Ile 900	Thr 900	Leu 900	Arg 900	Trp 905	Thr 905	Met 905	Gly 905	Phe 910	Asp 910	Asn 910
Ser 915	Pro 915	Ile 915	Thr 915	Gly 915	Tyr 915	Asp 915	Ile 920	Glu 920	Cys 920	Lys 920	Asn 920	Lys 925	Ser 925	Ser 925
Trp 930	Asp 930	Ser 930	Ala 930	Gln 930	Arg 930	Thr 935	Lys 935	Asp 935	Val 935	Ser 935	Pro 940	Gln 940	Leu 940	Ser 940

Ala Thr Ile Ile Asp Ile His Pro Ser Ser Thr Tyr Ser Ile Arg Met
 945 950 955 960
 Tyr Ala Lys Asn Arg Ile Gly Lys Ser Glu Pro Ser Asn Glu Leu Thr
 965 970 975
 Ile Thr Ala Asp Glu Ala Ala Pro Asp Gly Pro Pro Gln Glu Val His
 980 985 990
 Leu Glu Pro Ile Ser Ser Gln Ser Ile Arg Val Thr Trp Lys Ala Pro
 995 1000 1005
 Lys Lys His Leu Gln Asn Gly Ile Ile Arg Gly Tyr Gln Ile Gly Tyr
 1010 1015 1020
 Arg Glu Tyr Ser Thr Gly Gly Asn Phe Gln Phe Asn Ile Ile Ser Val
 1025 1030 1035 1040
 Asp Thr Ser Gly Asp Ser Glu Val Tyr Thr Leu Asp Asn Leu Asn Lys
 1045 1050 1055
 Phe Thr Gln Tyr Gly Leu Val Val Gln Ala Cys Asn Arg Ala Gly Thr
 1060 1065 1070
 Gly Pro Ser Ser Gln Glu Ile Ile Thr Thr Thr Leu Glu Asp Val Pro
 1075 1080 1085
 Ser Tyr Pro Pro Glu Asn Val Gln Ala Ile Ala Thr Ser Pro Glu Ser
 1090 1095 1100
 Ile Ser Ile Ser Trp Ser Thr Leu Ser Lys Glu Ala Leu Asn Gly Ile
 1105 1110 1115 1120
 Leu Gln Gly Phe Arg Val Ile Tyr Trp Ala Asn Leu Met Asp Gly Glu
 1125 1130 1135
 Leu Gly Glu Ile Lys Asn Ile Thr Thr Thr Gln Pro Ser Leu Glu Leu
 1140 1145 1150
 Asp Gly Leu Glu Lys Tyr Thr Asn Tyr Ser Ile Gln Val Leu Ala Phe
 1155 1160 1165
 Thr Arg Ala Gly Asp Gly Val Arg Ser Glu Gln Ile Phe Thr Arg Thr
 1170 1175 1180
 Lys Glu Asp Val Pro Gly Pro Pro Ala Gly Val Lys Ala Ala Ala Ala
 1185 1190 1195 1200
 Ser Ala Ser Met Val Phe Val Ser Trp Leu Pro Pro Leu Lys Leu Asn
 1205 1210 1215
 Gly Ile Ile Arg Lys Tyr Thr Val Phe Cys Ser His Pro Tyr Pro Thr
 1220 1225 1230
 Val Ile Ser Glu Phe Glu Ala Ser Pro Asp Ser Phe Ser Tyr Arg Ile
 1235 1240 1245
 Pro Asn Leu Ser Arg Asn Arg Gln Tyr Ser Val Trp Val Val Ala Val
 1250 1255 1260
 Thr Ser Ala Gly Arg Gly Asn Ser Ser Glu Ile Ile Thr Val Glu Pro
 1265 1270 1275 1280

00956994 1023
 46E201 16695680

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGGGTATTC TTACTCATGA GCATTTTCAGC TAAACTCTTT GCATCTCGCA GCCTCTTTAG	60
CCTCTGCTCC CGCCGCCTCC TCCGCACAAC CAGCAGGAGC ACAAACAGCA GCAAGACCCC	120
CACCAGGATA CAGGAGATGG TCACCAGCAT CTTGAGCCCC TCGTTGGTCG TCAGCCCTTC	180
TTCGTTTTTG ACAACTGACT TAATGAGTGG AGGAATTGTA CTGCCATCGT AGTTCAGCGT	240
AGCGAAGTTG GCCTGCTTCT CCGCGCAGCC CGCACTGTTG CACACCCGCA TCTGCAGCTC	300
ATACCAGGTG GCTTCCTGCA GGTACATACAG GATGTAGGAC TTGGAGAGAG AGGTCCTCTG	360
AGCTGTGGTC CAAACTGTGG TCCCAAAG	388

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTGATGCTC GAGTGAATTC	20
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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAGTTCTCA AAGGAGCAGG	20
-----------------------	----

46307 T69630

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 842 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCGGGCCCGGG	CGCGGCGGAG	CGCAGCGCAA	CGCGGGGGGC	GAGGCCGGCG	CGTGGCTCGC	60
TCGCTGGCTC	GCTGGCTCGC	GGGAGGCCGG	GCAGCAGCAG	GGGCATGTGG	ATACTGGCTC	120
TCTCCTTGTT	CCAGAGCTTC	GCGAATGTTT	TCAGTGAAGA	GCCCCACTCC	AGCCTCTACT	180
TTGTCAATGC	ATCGCTGCAA	GAGGTAGTGT	TTGCAAGCAC	ATCGGGGACG	CTGGTGCCCT	240
GCCCGGCTGC	AGGCATCCCT	CCTGTGACTC	TCAGATGGTA	CCTAGCAACG	GGCGAGGAGA	300
TCTACGATGT	CCCCGGGATC	CGCCACGTCC	ATCCCAATGG	CACTCTCCAA	ATTTTCCCCT	360
TTCCTCCTTC	AAGCTTCAGC	ACCTTAATCC	ATGATAATAC	TTACTATTGC	ACAGCTGAAA	420
ACCCTTCAGG	GAAAATTAGA	AGTCAGGATG	TCCACATCAA	GGCTGTTTTA	CGGGAGCCCT	480
ATACAGTCCG	TGTGGAGGAC	CAGAAAACCA	TGAGAGGCAA	TGTCGCGGTG	TTCAAGTGCA	540
TTATCCCCTC	CTCGGTGGAG	GCGTACGTCT	CTGTCTGTCTC	ATGGGAGAAA	GACACGGTTT	600
CACTTGTCTC	AGGATCTAGA	TTTCTCATCA	CATCCACGGG	AGCCTTGTAT	ATTAAAGATG	660
TTCAGAACGA	AGATGGGCTG	TACAAC TACC	GCTGCATCGC	GCGGCACAGA	TTCGCGGGGG	720
AGACGAGACA	GAGCAACTGC	GCGAGACTGT	TCGTGTCAGA	ACCAGCAAAC	TCAGCCCATC	780
CATCCTGGAA	GGGTTTGACC	ACCGCCAAAC	CATGGCCGGG	CACGCGTGGA	GCTGCCTTGC	840
CA						842

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 898 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGCCGGCCGG	TTGCAAGCCT	GTACTACAGG	CCATACTGCG	TGAATTATCA	GGTTGTCCAG	60
GGTGTACACT	TCGCTGTCCC	GGTGGTGTCA	ATACTGATGA	TGTTGAACTG	GAAGTTACCC	120
CGTGCTGTAC	TCCGGTAGCC	TATTGGTAGC	CGCGAATGAT	CCCGTCTTGT	ATAGTGTTCT	180
TGGGAGCCTC	TCCAGGTAAC	CCTGATACTC	TGAGATGAGG	TGGGTTCCAA	GTGAACTTCC	240
TGAGGTGGAC	ATCACGAGCT	GCCTCATCCG	CCGTGATGGT	GATCTCGTTG	CTGGGCTCAC	300
TCTTGCCAAT	CCGGTTCTTG	GCGTACATGC	GGATGCTGTA	GGTGGAGGAA	GGGTGGATAT	360
CAATGATGGT	GGCCGAGTTC	AGCTGAGGGG	AAACATCTTT	GGTTCTCTGA	GCAGAATCCC	420
ACGAGTCTGA	TTTATTTTGT	CATTCACT	GTCATAGCCT	GTGATGGGGC	TGTTGCCATC	480
AAACCCCATG	GTCCACCTGA	GCGTGATGGT	GCGAGCTTTG	ACATCTCTTG	ATCTCAATCT	540
CGGGAGGATC	TGGGGGTTCT	TGCACTGTGA	GTTGAATTAT	TCCACGGTCC	TCCCCGTATG	600
AATTGATAGC	ATGGCAGGAG	AAGAAACCGG	AATCTTCTCT	CACTGTTGGC	AAAATCTGCA	660
GCGTAGATAT	CACTTCCTCT	CCCACCTCCT	TGGTGGATAC	AGTACGGGCC	ACTTTCAGGG	720
TTAATGATCC	TGTCTCTCTT	CTCCAGCGGA	CAATGATGGG	CTCTCCCATG	GGCTGTGCAG	780
CTCATTCCTT	CCTTTGACCC	TGATGGCCAG	GTGGTGTGGG	TATAAGTTAT	ATCATGGCCC	840
GAATTTCCCT	GTGAGTCCAT	GGAATTGCTG	AACGTTCTGC	GCCCACATCG	TTGCTGA	898

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACCACCATTC	ACACACCCAG	ACATGGCGGG	TTGCGGCAA	CCTTCAGTTC	CTGGCCTTCC	60
TGTAGGGTAA	AGGGCTGCTG	CGGGTTTATA	GACCGGCACA	TGCCCATCCT	GGCATACGGT	120
GGCCAGTGGC	TTTCCATCTG	GATTCCAGGC	CAAGCTAAAA	ATCTGTTTCT	GATGGCCCTG	180

CAGTTTCAGC	CGTTCAGCTC	CAGTCTGAAG	TTCCCAGATG	CGAACGGTTA	GATCATAGGA	240
ACTGGAAGCC	AGTACATCGG	CAGCCAGGGG	GTGGAAGCGC	AGAGAGTAGA	TCTTTTCTGT	300
GTGGCCTGTG	AGCACAGTCT	CAGGTGTGGT	GAGAACATTC	TCGAGCCAGC	GAGCGTTCAT	360
ACCGCTTGGA	AAACCTAAAG	TGTGGGACTT	GGTATAAGTT	CACCCTTACT	GCCCCAAAATG	420
GAGTAGGTCC	CGGGCGCATA	AGTGAAATCA	TAGAAGCCAA	AACCCTGGGG	AAAGAACCCC	480
AGTTCTCCAA	GGAGCAGGAG	CTTTTCGCCA	GCATCAATAC	CACCCGAGTG	AGGCTGAATC	540
TGATTGGCTG	GAATGACGGC	GGCTGTCCAA	TCACCTCATT	CACTCTTGAA	TACAGACCCT	600
TTGGGACCAC	GGTCTGGACC	ACAGCTCAGC	GGACCTCCCT	TTCCAAGTCC	TAACATTCTG	660
TATGACCTGC	AAGAAGCCAC	GTGGTATGAA	CTGCAGATGA	GAGTGTGCAA	CAGCGCCGGC	720
TGTGCGGATA	AGCAAGCCAA	CTTCGCCACG	CTGAACTACG	ATGGCAGTAC	AATCCCTCCA	780
CTCATTAAGT	CAGTTGTCCA	CAAAGCGAAG	AAGGGCTGAC	AACCAACGAA	GGGCTCAAGA	840
TCCTCGTGAC	CATCTCCTGC	ATCCTGGTCG	GGGTTCTACT	GCTCTTTGTG	CTTCTGCTGG	900
TTGTGCGGAG	GAGACGGCGA	GAGCAGAGGC	TGAAGAGGCT	GAGAGATGCA	AAGAGTTTAG	960
CTGAAATGCT	CATGAGCAAA	AACACACGGA	CTTCAGATAC	CTTAAGCAAA	CAGCAGCAGA	1020
CTTTGAGAAT	GCACATTGAT	ATACCCAGGG	CTCAGCTTTT	GATTGAAGAG	AGAGACACAA	1080
TGGAGACCAT	AGATGACCGC	TCCACAGTCC	TGTTGACGGA	TGCTGACTTC	GGGGAGGCAG	1140
CCAAACAGAA	GTCACTGACA	GTGACTCACA	CGGTGCATTA	CCAATCGGTG	TCTCAGGCCA	1200
CCGGGCCCCCT	CGTGGATGTC	TCCGATGCTC	GGCCAGGAAC	GAATCCCACC	ACCAGGAGGA	1260
ATGCAAAGGC	TGGACCCACA	GCGAGAAACC	GGTACGCCAG	CCAGTGGACG	CTCAACAGAC	1320
CCCATCCTAC	CATCTCTGCA	CACACCCTCA	CCACAGAATG	AGACTGCTAC	ACCAGGCTAC	1380
AGGATCCGTG	ACAGGAGAGC	GACAGTACAG	CGTCAGCCCA	TTCACAAGAC	ACAGACGAGC	1440
AAGAAGCAGC	ATGTTCTCCA	CAGAAAGTGC	TTCTTCTACC	TACGAAGACT	GCCAGGCCTA	1500
TGAACACGCC	AAGATGGAAG	AGCAGCTGAG	GCATGCCAAG	TTCACCATCA	CAGAGTGCTT	1560
CATATCCGAT	ACGTCCTCCG	AGCAGTTGAC	GGCAGGACAA	ATGAGTACAC	GGACAGTCTG	1620
ACTCCAGTAC	CCCTTCAGAA	TCGGGATCTG	CAGATTCATG	CATCTCCCCC	CAACCTCAGG	1680
ATGGAGGACG	AGTGTGAACA	TGGCGGTTCC	AAAGGCCCAT	CGGCCAGGCG	ACTCATAAC	1740
CTGCTCCATA	CCTACGATGG	ATTCTTGTTA	AACCGGGCGC	ACCAGGCACC	AGCAGGACTG	1800
AGTTTAGGAC	AAGCGTGCTT	GGAACCCAG	AAAGTCGGAC	CCTGAAACGC	CCCACGGTCG	1860
TTGAGCCCAC	CCCTATGGAG	GCCTCCTCCT	CCACTTCTTC	CACGCGAGAA	GGACAGCAGT	1920
CGTGGAACA	AGGGGCTGTG	GCCACCTTAC	CTCAGCGAGA	GGGTGCAGAG	CTGGACAGGC	1980
AGCTAAAATG	AGCAGCTCCC	AAGAGTCACT	GCTGGACTCC	CGGGCCATTG	AAAGGAACAA	2040
TCCCTACGCA	AATCTTACAC	CTTGGTATAA	CACATGGCAC	TGATGGACAG	CGGTTGTAAT	2100

ACAATTAACG AGCCAATCAA GCTACTTTTT TATGAATTCC GATATTTATA ATTAAGAATT 2160
GCCAAATATA TTA 2173

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 453..5168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGACTGAGGC CGGAGCACGG CAAAGATGAG CCTGCCCCGCC CGCCTGCTGC CTGGATGCGG	60
AGGGTGAGGG CTGGCGCACG GGAGGCCGCT GGCTGCGCAT TCTGGGCGCC GAGTGCCCGG	120
GATGAGCTCA CGCCCGCGTC TCGGCTCTC TCCACCTGCC GACCTGCCGG GGGCCCACTG	180
AGCTGACGGC GCACCTGGGC TCCGGCCGCA GCGTGGGGCG CGGCGCCCGG GAGCAGGTGT	240
GCAGGAGCGC AGCGCGCGGC GAGCGCAGCC CTCGCTCCGG AGCCCGGCCG CGCCGCGTGC	300
CCGGGCGGGCT AGGCAGCGGC GCGGCGGGCG GCGGGCGGGC GGCGGGCGGC GGCCCCGGG	360
CAGGTGCCGA GCGGCGAGCG GAGCCGGGCC GGGCGGAGCG CGGGGGGCGA GGCCGGCGCG	420
TCGCTCGCGG GAGGCCGGGG AGCGGCAGGG GC ATG TGG ATA CTG GCT CTC TCC	473
Met Trp Ile Leu Ala Leu Ser	
1 5	
TTG TTC CAG AGC TTC GCG AAT GTT TTC AGT GAA GAC CTA CAC TCC AGC	521
Leu Phe Gln Ser Phe Ala Asn Val Phe Ser Glu Asp Leu His Ser Ser	
10 15 20	
CTC TAC TTT GTC AAT GCA TCT CTG CAA GAG GTA GTG TTT GCC AGC ACC	569
Leu Tyr Phe Val Asn Ala Ser Leu Gln Glu Val Val Phe Ala Ser Thr	
25 30 35	
ACG GGG ACT CTG GTG CCC TGC CCC GCA GCA GGC ATC CCT CCT GTG ACT	617
Thr Gly Thr Leu Val Pro Cys Pro Ala Ala Gly Ile Pro Pro Val Thr	
40 45 50 55	
CTC AGA TGG TAC CTA GCC ACG GGC GAG GAG ATC TAC GAT GTC CCC GGG	665
Leu Arg Trp Tyr Leu Ala Thr Gly Glu Glu Ile Tyr Asp Val Pro Gly	
60 65 70	
ATC CGC CAC GTC CAC CCC AAC GGC ACT CTC CAA ATT TTC CCC TTC CCT	713
Ile Arg His Val His Pro Asn Gly Thr Leu Gln Ile Phe Pro Phe Pro	
75 80 85	
CCT TCA AGC TTC AGT ACC TTA ATC CAT GAT AAT ACT TAT TAT TGC ACA	761
Pro Ser Ser Phe Ser Thr Leu Ile His Asp Asn Thr Tyr Tyr Cys Thr	
90 95 100	

08956991-102397

GCT	GAA	AAT	CCT	TCA	GGG	AAA	ATT	AGA	AGT	CAG	GAT	GTC	CAC	ATC	AAG	809
Ala	Glu	Asn	Pro	Ser	Gly	Lys	Ile	Arg	Ser	Gln	Asp	Val	His	Ile	Lys	
105						110					115					
GCT	GTT	TTA	CGG	GAG	CCC	TAT	ACA	GTC	CGT	GTG	GAG	GAC	CAG	AAA	ACC	857
Ala	Val	Leu	Arg	Glu	Pro	Tyr	Thr	Val	Arg	Val	Glu	Asp	Gln	Lys	Thr	
120					125					130					135	
ATG	AGA	GGC	AAT	GTT	GCG	GTC	TTC	AAG	TGC	ATT	ATC	CCC	TCC	TCG	GTG	905
Met	Arg	Gly	Asn	Val	Ala	Val	Phe	Lys	Cys	Ile	Ile	Pro	Ser	Ser	Val	
				140					145					150		
GAG	GCG	TAC	ATC	ACT	GTC	GTC	TCA	TGG	GAG	AAA	GAC	ACT	GTT	TCA	CTT	953
Glu	Ala	Tyr	Ile	Thr	Val	Val	Ser	Trp	Glu	Lys	Asp	Thr	Val	Ser	Leu	
			155					160					165			
GTC	TCA	GGA	TCT	AGA	TTT	CTC	ATC	ACA	TCC	ACG	GGA	GCC	TTG	TAT	ATT	1001
Val	Ser	Gly	Ser	Arg	Phe	Leu	Ile	Thr	Ser	Thr	Gly	Ala	Leu	Tyr	Ile	
		170				175						180				
AAA	GAT	GTA	CAG	AAT	GAA	GAT	GGA	TTG	TAT	AAC	TAC	CGC	TGC	ATC	ACG	1049
Lys	Asp	Val	Gln	Asn	Glu	Asp	Gly	Leu	Tyr	Asn	Tyr	Arg	Cys	Ile	Thr	
185						190					195					
CGG	CAT	CGA	TAC	ACC	GGA	GAG	ACG	AGG	CAG	AGC	AAC	AGC	GCC	AGA	CTT	1097
Arg	His	Arg	Tyr	Thr	Gly	Glu	Thr	Arg	Gln	Ser	Asn	Ser	Ala	Arg	Leu	
200					205					210					215	
TTT	GTA	TCA	GAC	CCA	GCG	AAC	TCA	GCC	CCA	TCC	ATA	CTG	GAT	GGG	TTT	1145
Phe	Val	Ser	Asp	Pro	Ala	Asn	Ser	Ala	Pro	Ser	Ile	Leu	Asp	Gly	Phe	
				220					225					230		
GAC	CAT	CGC	AAA	GCC	ATG	GCT	GGG	CAG	CGT	GTG	GAG	CTG	CCT	TGC	AAA	1193
Asp	His	Arg	Lys	Ala	Met	Ala	Gly	Gln	Arg	Val	Glu	Leu	Pro	Cys	Lys	
			235					240					245			
GCG	CTC	GGG	CAC	CCT	GAG	CCA	GAT	TAC	CGC	TGG	CTG	AAG	GAC	AAC	ATG	1241
Ala	Leu	Gly	His	Pro	Glu	Pro	Asp	Tyr	Arg	Trp	Leu	Lys	Asp	Asn	Met	
		250					255					260				
CCC	CTG	GAA	CTT	TCA	GGG	AGG	TTC	CAG	AAG	ACC	GTG	ACG	GGG	CTG	CTC	1289
Pro	Leu	Glu	Leu	Ser	Gly	Arg	Phe	Gln	Lys	Thr	Val	Thr	Gly	Leu	Leu	
		265				270					275					
ATT	GAG	AAC	ATT	CGC	CCC	TCG	GAC	TCA	GGC	AGC	TAT	GTT	TGT	GAA	GTG	1337
Ile	Glu	Asn	Ile	Arg	Pro	Ser	Asp	Ser	Gly	Ser	Tyr	Val	Cys	Glu	Val	
280					285					290					295	
TCC	AAC	AGA	TAC	GGA	ACT	GCT	AAG	GTG	ATA	GGC	CGC	CTG	TAC	GTG	AAA	1385
Ser	Asn	Arg	Tyr	Gly	Thr	Ala	Lys	Val	Ile	Gly	Arg	Leu	Tyr	Val	Lys	
				300					305					310		
CAG	CCA	CTG	AAA	GCC	ACC	ATC	AGT	CCC	AGG	AAG	GTT	AAA	AGC	AGC	GTG	1433
Gln	Pro	Leu	Lys	Ala	Thr	Ile	Ser	Pro	Arg	Lys	Val	Lys	Ser	Ser	Val	
			315					320					325			
GGT	AGC	CAA	GTT	TCC	TTG	TCC	TGC	AGC	GTG	ACA	GGA	ACT	GAG	GAC	CAG	1481
Gly	Ser	Gln	Val	Ser	Leu	Ser	Cys	Ser	Val	Thr	Gly	Thr	Glu	Asp	Gln	
		330					335					340				
GAA	CTC	TCC	TGG	TAC	CGC	AAT	GGT	GAA	ATC	CTC	AAC	CCT	GGA	AAA	AAT	1529
Glu	Leu	Ser	Trp	Tyr	Arg	Asn	Gly	Glu	Ile	Leu	Asn	Pro	Gly	Lys	Asn	
		345				350					355					

GTG Val 360	AGG Arg	ATC Ile	ACA Thr	GGG Gly 365	ATC Ile 365	AAC Asn	CAC His	GAA Glu	AAC Asn	CTT Leu 370	ATA Ile	ATG Met	GAT Asp	CAC His	ATG Met 375	1577
GTC Val	AAA Lys	AGT Ser	GAC Asp	GGG Gly 380	GGC Gly	GCA Ala	TAC Tyr	CAG Gln	TGC Cys 385	TTT Phe	GTG Val	CGC Arg	AAG Lys	GAC Asp 390	AAG Lys	1625
CTG Leu	TCC Ser	GCT Ala	CAA Gln 395	GAC Asp	TAT Tyr	GTG Val	CAG Gln	GTG Val 400	GTC Val	CTT Leu	GAA Glu	GAT Asp	GGA Gly 405	ACT Thr	CCC Pro	1673
AAA Lys	ATT Ile	ATT Ile 410	TCT Ser	GCC Ala	TTT Phe	AGT Ser	GAA Glu 415	AAG Lys	GTG Val	GTG Val	AGT Ser	CCA Pro 420	GCA Ala	GAG Glu	CCG Pro	1721
GTT Val	TCC Leu 425	CTT Leu	ATG Met	TGC Cys	AAC Asn 430	GTG Val	AAG Lys	GGA Gly	ACA Thr	CCT Pro 435	TTG Leu	CCC Pro	ACG Thr	ATC Ile	ACG Thr	1769
TGG Trp 440	ACC Thr	CTG Leu	GAC Asp	GAT Asp 445	GAC Asp	CCG Pro	ATT Ile	CTC Leu	AAG Lys	GGT Gly 450	GGC Gly	AGT Ser	CAC His	CGC Arg	ATC Ile 455	1817
AGC Ser	CAG Gln	ATG Met	ATC Ile	ACG Thr 460	TCG Ser	GAG Glu	GGG Gly	AAC Asn 465	GTG Val	GTC Val	AGC Ser	TAC Tyr	CTG Leu	AAC Asn 470	ATC Ile	1865
TCC Ser	AGC Ser	TCC Ser	CAG Gln 475	GTC Val	CGG Arg	GAC Asp	GGG Gly	GGA Gly 480	GTC Val	TAC Tyr	CGC Arg	TGC Cys	ACT Thr 485	GCC Ala	AAC Asn	1913
AAC Asn	TCG Ser 490	GCG Ala	GGA Gly	GTC Val	GTC Val	CTG Leu	TAC Tyr 495	CAG Gln	GCT Ala	CGA Arg	ATA Ile	AAC Asn 500	GTA Val	AGA Arg	GGG Gly	1961
CCT Pro 505	GCA Ala	AGC Ser	ATT Ile	CGA Arg	CCA Pro	ATG Met 510	AAA Lys	AAC Asn	ATC Ile	ACA Thr	GCA Ala 515	ATA Ile	GCA Ala	GGA Gly	CGG Arg	2009
GAC Asp 520	ACA Thr	TAC Tyr	ATT Ile	CAC His	TGT Cys 525	CGT Arg	GTG Val	ATT Ile	GGC Gly	TAT Tyr 530	CCG Pro	TAT Tyr	TAC Tyr	TCC Ser	ATT Ile 535	2057
AAA Lys	TGG Trp	TAC Tyr	AAG Lys	AAC Asn 540	TCT Ser	AAC Asn	CTG Leu	CTT Leu	CCT Pro 545	TTC Phe	AAC Asn	CAC His	CGC Arg	CAA Gln 550	GTG Val	2105
GCA Ala	TTT Phe	GAG Glu	AAC Asn 555	AAT Asn	GGA Gly	ACT Thr	CTT Leu	AAA Lys 560	CTT Leu	TCA Ser	GAT Asp	GTG Val	CAA Gln 565	AAG Lys	GAA Glu	2153
GTG Val	GAC Asp 570	GAG Glu	GGG Gly	GAG Glu	TAC Tyr	ACG Thr	TGC Cys 575	AAC Asn	GTG Val	TTG Leu	GTT Val	CAA Gln 580	CCA Pro	CAA Gln	CTC Leu	2201
TCC Ser 585	ACC Thr	AGC Ser	CAG Gln	AGC Ser	GTC Val	CAC His 590	GTG Val	ACC Thr	GTG Val	AAA Lys 595	GTT Val	CCG Pro	CCT Pro	TTC Phe	ATA Ile	2249
CAA Gln 600	CCC Pro	TTT Phe	GAG Glu	TTT Phe	CCA Pro 605	AGA Arg	TTC Phe	TCC Ser	ATT Ile	GGG Gly 610	CAG Gln	CGG Arg	GTC Val	TTC Phe	ATC Ile 615	2297

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CCC Pro	TGT Cys	GTT Val	GTG Val	GTC Val 620	TCA Ser	GGG Gly	GAC Asp	TTA Leu	CCC Pro 625	ATC Ile	ACG Thr	ATC Ile	ACC Thr	TGG Trp 630	CAG Gln	2345
AAG Lys	GAT Asp	GGC Gly	CGG Arg 635	CCA Pro	ATC Ile	CCT Pro	GGG Gly	AGC Ser 640	CTT Leu	GGG Gly	GTG Val	ACC Thr	ATT Ile 645	GAC Asp	AAT Asn	2393
ATT Ile	GAC Asp	TTC Phe 650	ACG Thr	AGC Ser	TCC Ser	TTG Leu	AGG Arg 655	ATT Ile	TCC Ser	AAT Asn	CTC Leu	TGC Ser 660	CTC Leu	ATG Met	CAC His	2441
AAT Asn	GGG Gly 665	AAT Asn	TAC Tyr	ACC Thr	TGC Cys	ATA Ile 670	GCC Ala	CGG Arg	AAT Asn	GAG Glu	GCC Ala 675	GCC Ala	GCT Ala	GTG Val	GAG Glu	2489
CAC His 680	CAA Gln	AGC Ser	CAG Gln	TTG Leu	ATT Ile 685	GTC Val	AGA Arg	GTT Val	CCT Pro	CCC Pro 690	AAG Lys	TTT Phe	GTG Val	GTT Val	CAG Gln 695	2537
CCA Pro	CGG Arg	GAC Asp	CAG Gln	GAC Asp 700	GGG Gly	ATT Ile	TAT Tyr	GGC Gly	AAA Lys 705	GCA Ala	GTC Val	ATC Ile	CTC Leu	AAT Asn 710	TGT Cys	2585
TCT Ser	GCT Ala	GAG Glu	GGT Gly 715	TAC Tyr	CCT Pro	GTA Val	CCT Pro	ACC Thr 720	ATC Ile	GTG Val	TGG Trp	AAA Lys	TTC Phe 725	TCT Ser	AAA Lys	2633
GGT Gly	GCT Ala	GGG Gly 730	GTT Val	CCC Pro	CAG Gln	TTC Phe	CAG Gln 735	CCA Pro	ATT Ile	GCC Ala	CTA Leu	AAT Asn 740	GGC Gly	CGA Arg	ATC Ile	2681
CAA Gln	GTT Val 745	CTC Leu	AGC Ser	AAT Asn	GGG Gly	TCG Ser 750	TTG Leu	CTG Leu	ATC Ile	AAG Lys	CAT His 755	GTC Val	GTG Val	GAG Glu	GAA Glu	2729
GAC Asp 760	AGT Ser	GGC Gly	TAC Tyr	TAC Tyr	CTC Leu 765	TGC Cys	AAG Lys	GTC Val	AGC Ser	AAC Asn 770	GAT Asp	GTG Val	GGC Gly	GCA Ala	GAC Asp 775	2777
GTC Val	AGC Ser	AAG Lys	TCC Ser	ATG Met 780	TAC Tyr	CTC Leu	ACG Thr	GTT Val	AAA Lys 785	ATT Ile	CCT Pro	GCG Ala	ATG Met	ATA Ile 790	ACA Thr	2825
TCC Ser	TAT Tyr	CCA Pro	AAT Asn 795	ACT Thr	ACC Thr	CTG Leu	GCC Ala	ACG Thr 800	CAG Gln	GGG Gly	CAG Gln	AAA Lys	AAG Lys 805	GAG Glu	ATG Met	2873
AGC Ser	TGC Cys	ACG Thr 810	GCG Ala	CAT His	GGT Gly	GAG Glu	AAG Lys 815	CCC Pro	ATT Ile	ATA Ile	GTC Val	CGC Arg 820	TGG Trp	GAG Glu	AAG Lys	2921
GAG Glu	GAC Asp 825	CGA Arg	ATC Ile	ATT Ile	AAC Asn	CCT Pro 830	GAG Glu	ATG Met	GCC Ala	CGT Arg	TAT Tyr 835	CTT Leu	GTG Val	TCC Ser	ACC Thr	2969
AAG Lys 840	GAG Glu	GTG Val	GGA Gly	GAA Glu	GAG Glu 845	GTG Val	ATT Ile	TCT Ser	ACT Thr	CTG Leu 850	CAG Gln	ATT Ile	TTG Leu	CCA Pro	ACT Thr 855	3017
GTG Val	AGA Arg	GAA Glu	GAT Asp	TCT Ser 860	GGT Gly	TTC Phe	TTT Phe	TCC Ser	TGC Cys 865	CAT His	GCT Ala	ATT Ile	AAT Asn	TCT Ser 870	TAT Tyr	3065

GGG Gly	GAG Glu	GAC Asp	CGT Arg	GGA Gly	ATA Ile	ATT Ile	CAG Gln	CTC Leu	ACA Thr	GTG Val	CAA Gln	GAG Glu	CCC Pro	CCA Pro	GAC Asp	3113
			875					880					885			
CCT Pro	CCC Pro	GAA Glu	ATT Ile	GAG Glu	ATC Ile	AAA Lys	GAT Asp	GTC Val	AAA Lys	GCA Ala	CGC Arg	ACA Thr	ATT Ile	ACG Thr	CTC Leu	3161
		890					895					900				
AGG Arg	TGG Trp	ACC Thr	ATG Met	GGG Gly	TTT Phe	GAT Asp	GGA Gly	AAC Asn	AGT Ser	CCC Pro	ATC Ile	ACA Thr	GGC Gly	TAC Tyr	GAT Asp	3209
	905					910					915					
ATT Ile	GAA Glu	TGC Cys	AAA Lys	AAT Asn	AAA Lys	TCA Ser	GAC Asp	TCC Ser	TGG Trp	GAT Asp	TCT Ser	GCT Ala	CAG Gln	AGA Arg	ACC Thr	3257
	920				925					930					935	
AAA Lys	GAT Asp	GTT Val	TCC Ser	CCT Pro	CAG Gln	CTG Leu	AAC Asn	TCG Ser	GCC Ala	ACC Thr	ATC Ile	ATT Ile	GAT Asp	ATC Ile	CAC His	3305
				940					945						950	
CCT Pro	TCC Ser	TCC Ser	ACC Thr	TAC Tyr	AGC Ser	ATC Ile	CGC Arg	ATG Met	TAC Tyr	GCC Ala	AAG Lys	AAC Asn	CGG Arg	ATT Ile	GGC Gly	3353
			955					960					965			
AAG Lys	AGC Ser	GAG Glu	CCC Pro	AGC Ser	AAC Asn	GAG Glu	CTC Leu	ACC Thr	ATC Ile	ACG Thr	GCG Ala	GAC Asp	GAG Glu	GCA Ala	GCT Ala	3401
		970					975					980				
CCT Pro	GAT Asp	GGT Gly	CCA Pro	CCT Pro	CAG Gln	GAA Glu	GTT Val	CAC His	CTG Leu	GAG Glu	CCT Pro	ATA Ile	TCA Ser	TCT Ser	CAG Gln	3449
	985					990					995					
AGC Ser	ATC Ile	AGG Arg	GTC Val	ACA Thr	TGG Trp	AAG Lys	GCT Ala	CCC Pro	AAG Lys	AAA Lys	CAT His	TTG Leu	CAA Gln	AAT Asn	GGG Gly	3497
	1000				1005					1010					1015	
ATT Ile	ATC Ile	CGT Arg	GGC Gly	TAC Tyr	CAA Gln	ATA Ile	GGT Gly	TAC Tyr	CGA Arg	GAG Glu	TAC Tyr	AGC Ser	ACT Thr	GGG Gly	GGT Gly	3545
				1020					1025					1030		
AAC Asn	TTC Phe	CAA Gln	TTC Phe	AAC Asn	ATT Ile	ATC Ile	AGT Ser	GTC Val	GAC Asp	ACC Thr	AGC Ser	GGG Gly	GAC Asp	AGT Ser	GAG Glu	3593
			1035					1040					1045			
GTT Val	TAC Tyr	ACC Thr	CTG Leu	GAC Asp	AAC Asn	CTG Leu	AAT Asn	AAG Lys	TTC Phe	ACT Thr	CAG Gln	TAC Tyr	GGC Gly	CTG Leu	GTG Val	3641
		1050					1055					1060				
GTG Val	CAG Gln	GCC Ala	TGT Cys	AAC Asn	CGG Arg	GCC Ala	GGC Gly	ACG Thr	GGG Gly	CCT Pro	TCT Ser	TCT Ser	CAG Gln	GAA Glu	ATC Ile	3689
	1065					1070					1075					
ATC Ile	ACC Thr	ACC Thr	ACT Thr	CTC Leu	GAG Glu	GAT Asp	GTG Val	CCC Pro	AGT Ser	TAC Tyr	CCC Pro	CCC Pro	GAA Glu	AAT Asn	GTC Val	3737
	1080				1085					1090					1095	
CAA Gln	GCC Ala	ATA Ile	GCA Ala	ACA Thr	TCA Ser	CCA Pro	GAA Glu	AGC Ser	ATA Ile	TCA Ser	ATA Ile	TCC Ser	TGG Trp	TCC Ser	ACA Thr	3785
				1100					1105					1110		
CTT Leu	TCC Ser	AAG Lys	GAA Glu	GCC Ala	TTG Leu	AAT Asn	GGA Gly	ATT Ile	CTC Leu	CAG Gln	GGG Gly	TTC Phe	AGA Arg	GTC Val	ATT Ile	3833
			1115					1120					1125			

TAC TGG GCC AAC CTC ATG GAC GGA GAG CTG GGT GAG ATT AAA AAC ATC Tyr Trp Ala Asn Leu Met Asp Gly Glu Leu Gly Glu Ile Lys Asn Ile 1130 1135 1140	3881
ACC ACC ACA CAG CCT TCA CTG GAG CTG GAC GGG CTG GAA AAG TAC ACC Thr Thr Thr Gln Pro Ser Leu Glu Leu Asp Gly Leu Glu Lys Tyr Thr 1145 1150 1155	3929
AAC TAC AGC ATC CAG GTG CTG GCC TTC ACC CGC GCA GGA GAC GGG GTC Asn Tyr Ser Ile Gln Val Leu Ala Phe Thr Arg Ala Gly Asp Gly Val 1160 1165 1170 1175	3977
AGG AGT GAG CAG ATC TTC ACC CGG ACC AAA GAG GAT GTT CCA GGT CCT Arg Ser Glu Gln Ile Phe Thr Arg Thr Lys Glu Asp Val Pro Gly Pro 1180 1185 1190	4025
CCC GCG GGT GTG AAG GCA GCG GCG GCC TCA GCC TCC ATG GTC TTT GTG Pro Ala Gly Val Lys Ala Ala Ala Ser Ala Ser Met Val Phe Val 1195 1200 1205	4073
TCC TGG CTT CCC CCT CTC AAG CTG AAC GGC ATC ATC CGA AAG TAC ACT Ser Trp Leu Pro Pro Leu Lys Leu Asn Gly Ile Ile Arg Lys Tyr Thr 1210 1215 1220	4121
GTA TTC TGC TCC CAC CCC TAT CCC ACA GTG ATC AGC GAG TTT GAG GCC Val Phe Cys Ser His Pro Tyr Pro Thr Val Ile Ser Glu Phe Glu Ala 1225 1230 1235	4169
TCT CCC GAC TCG TTT TCC TAC AGA ATT CCC AAC CTG AGT AGG AAT CGT Ser Pro Asp Ser Phe Ser Tyr Arg Ile Pro Asn Leu Ser Arg Asn Arg 1240 1245 1250 1255	4217
CAG TAC AGC GTC TGG GTG GTG GCT GTT ACT TCA GCC GGA AGA GGC AAC Gln Tyr Ser Val Trp Val Val Ala Val Thr Ser Ala Gly Arg Gly Asn 1260 1265 1270	4265
AGC AGT GAA ATC ATC ACA GTC GAG CCA CTA GCA AAA GCT CCT GCA CGA Ser Ser Glu Ile Ile Thr Val Glu Pro Leu Ala Lys Ala Pro Ala Arg 1275 1280 1285	4313
ATC CTG ACC TTC AGT GGG ACA GTG ACT ACT CCA TGG ATG AAA GAC ATT Ile Leu Thr Phe Ser Gly Thr Val Thr Thr Pro Trp Met Lys Asp Ile 1290 1295 1300	4361
GTC TTG CCT TGT AAG GCT GTT GGG GAC CCT TCT CCT GCA GTC AAA TGG Val Leu Pro Cys Lys Ala Val Gly Asp Pro Ser Pro Ala Val Lys Trp 1305 1310 1315	4409
ATG AAA GAC AGT AAC GGG ACA CCC AGT CTA GTA ACG ATT GAT GGG CGG Met Lys Asp Ser Asn Gly Thr Pro Ser Leu Val Thr Ile Asp Gly Arg 1320 1325 1330 1335	4457
AGG AGC ATC TTT AGC AAC GGA AGC TTC ATT ATT CGC ACG GTG AAA GCA Arg Ser Ile Phe Ser Asn Gly Ser Phe Ile Ile Arg Thr Val Lys Ala 1340 1345 1350	4505
GAA GAC TCC GGC TAT TAC AGC TGC ATT GCC AAT AAC AAC TGG GGA TCT Glu Asp Ser Gly Tyr Tyr Ser Cys Ile Ala Asn Asn Asn Trp Gly Ser 1355 1360 1365	4553
GAT GAA ATT ATT TTA AAC TTA CAA GTA CAA GTT CCA CCA GAT CAG CCT Asp Glu Ile Ile Leu Asn Leu Gln Val Gln Val Pro Pro Asp Gln Pro 1370 1375 1380	4601

AGCAGCATGG TCTCCACAGA AAGTGCCTCC TCCACTTACG AAGAACTGGC CAGGGCCTAC 5715
 GAACACGCCA AGATGGAAGA GCAACTGAGG CACGCCAAGT TCACCATCAC GGAGTGCTTC 5775
 ATATCAGACA CGTCATCGGA GCAGTTGACG GCAGGGACAA ATGAGTACAC GGACAGTCTG 5835
 ACCTCCAGCA CCCCTTCCGA ATCGGGAATC TGCAGGTTCA CTGCATCTCC CCCCAAACCT 5895
 CAGGATGGAG GAAGAGTAAT GAATATGGCA GTTCCAAAGG CAATCGGCCA GGTGACCTCA 5955
 TACATTTGCC TCCATACCTT AGAATGGACT TTTTGTTAAA CCGAGGTGGT CCAGGCACCA 6015
 GCAGGGACCT GAGCTTAGGA CAAGCATGCT TGGAACCTCA GAAAAGCCGG ACCCTGAAGC 6075
 GCCCCACGGT CCTGGAGCCC ATCCCAGATGG AAGCCGCCTC CTCCGCCTCC TCCACGAGAG 6135
 AAGGACAGTC GTGGCAGCCG GGGGCCGTGG CCACATTACC TCAGCGGGAG GGAGCAGAGC 6195
 TGGGACAGGC AGCTAAAATG AGCAGCTCCC AAGAATCACT GCTCGACTCC CGGGGCCATT 6255
 TGAAAGGAAA CAATCCTTAC GCAAAATCTT ACACCCTGGT ATAACAGACA GCATGACTGG 6315
 ACAGCGGTTG TAAATACAAT TCAACAATT CAATCAAAGC TACCTTTTTT TTACGGAATT 6375
 CCAATATTTA TAATTAAAGA AAATTGCCAA AATATATT 6413

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1571 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Trp Ile Leu Ala Leu Ser Leu Phe Gln Ser Phe Ala Asn Val Phe
 1 5 10 15
 Ser Glu Asp Leu His Ser Ser Leu Tyr Phe Val Asn Ala Ser Leu Gln
 20 25 30
 Glu Val Val Phe Ala Ser Thr Thr Gly Thr Leu Val Pro Cys Pro Ala
 35 40 45
 Ala Gly Ile Pro Pro Val Thr Leu Arg Trp Tyr Leu Ala Thr Gly Glu
 50 55 60
 Glu Ile Tyr Asp Val Pro Gly Ile Arg His Val His Pro Asn Gly Thr
 65 70 75 80
 Leu Gln Ile Phe Pro Phe Pro Pro Ser Ser Phe Ser Thr Leu Ile His
 85 90 95
 Asp Asn Thr Tyr Tyr Cys Thr Ala Glu Asn Pro Ser Gly Lys Ile Arg
 100 105 110
 Ser Gln Asp Val His Ile Lys Ala Val Leu Arg Glu Pro Tyr Thr Val
 115 120 125

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Arg Val Glu Asp Gln Lys Thr Met Arg Gly Asn Val Ala Val Phe Lys
 130 135 140
 Cys Ile Ile Pro Ser Ser Val Glu Ala Tyr Ile Thr Val Val Ser Trp
 145 150 155 160
 Glu Lys Asp Thr Val Ser Leu Val Ser Gly Ser Arg Phe Leu Ile Thr
 165 170 175
 Ser Thr Gly Ala Leu Tyr Ile Lys Asp Val Gln Asn Glu Asp Gly Leu
 180 185 190
 Tyr Asn Tyr Arg Cys Ile Thr Arg His Arg Tyr Thr Gly Glu Thr Arg
 195 200 205
 Gln Ser Asn Ser Ala Arg Leu Phe Val Ser Asp Pro Ala Asn Ser Ala
 210 215 220
 Pro Ser Ile Leu Asp Gly Phe Asp His Arg Lys Ala Met Ala Gly Gln
 225 230 235 240
 Arg Val Glu Leu Pro Cys Lys Ala Leu Gly His Pro Glu Pro Asp Tyr
 245 250 255
 Arg Trp Leu Lys Asp Asn Met Pro Leu Glu Leu Ser Gly Arg Phe Gln
 260 265 270
 Lys Thr Val Thr Gly Leu Leu Ile Glu Asn Ile Arg Pro Ser Asp Ser
 275 280 285
 Gly Ser Tyr Val Cys Glu Val Ser Asn Arg Tyr Gly Thr Ala Lys Val
 290 295 300
 Ile Gly Arg Leu Tyr Val Lys Gln Pro Leu Lys Ala Thr Ile Ser Pro
 305 310 315 320
 Arg Lys Val Lys Ser Ser Val Gly Ser Gln Val Ser Leu Ser Cys Ser
 325 330 335
 Val Thr Gly Thr Glu Asp Gln Glu Leu Ser Trp Tyr Arg Asn Gly Glu
 340 345 350
 Ile Leu Asn Pro Gly Lys Asn Val Arg Ile Thr Gly Ile Asn His Glu
 355 360 365
 Asn Leu Ile Met Asp His Met Val Lys Ser Asp Gly Gly Ala Tyr Gln
 370 375 380
 Cys Phe Val Arg Lys Asp Lys Leu Ser Ala Gln Asp Tyr Val Gln Val
 385 390 395 400
 Val Leu Glu Asp Gly Thr Pro Lys Ile Ile Ser Ala Phe Ser Glu Lys
 405 410 415
 Val Val Ser Pro Ala Glu Pro Val Ser Leu Met Cys Asn Val Lys Gly
 420 425 430
 Thr Pro Leu Pro Thr Ile Thr Trp Thr Leu Asp Asp Asp Pro Ile Leu
 435 440 445
 Lys Gly Gly Ser His Arg Ile Ser Gln Met Ile Thr Ser Glu Gly Asn
 450 455 460

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Val Val Ser Tyr Leu Asn Ile Ser Ser Ser Gln Val Arg Asp Gly Gly
 465 470 475 480
 Val Tyr Arg Cys Thr Ala Asn Asn Ser Ala Gly Val Val Leu Tyr Gln
 485 490 495
 Ala Arg Ile Asn Val Arg Gly Pro Ala Ser Ile Arg Pro Met Lys Asn
 500 505 510
 Ile Thr Ala Ile Ala Gly Arg Asp Thr Tyr Ile His Cys Arg Val Ile
 515 520 525
 Gly Tyr Pro Tyr Tyr Ser Ile Lys Trp Tyr Lys Asn Ser Asn Leu Leu
 530 535 540
 Pro Phe Asn His Arg Gln Val Ala Phe Glu Asn Asn Gly Thr Leu Lys
 545 550 555 560
 Leu Ser Asp Val Gln Lys Glu Val Asp Glu Gly Glu Tyr Thr Cys Asn
 565 570 575
 Val Leu Val Gln Pro Gln Leu Ser Thr Ser Gln Ser Val His Val Thr
 580 585 590
 Val Lys Val Pro Pro Phe Ile Gln Pro Phe Glu Phe Pro Arg Phe Ser
 595 600 605
 Ile Gly Gln Arg Val Phe Ile Pro Cys Val Val Val Ser Gly Asp Leu
 610 615 620
 Pro Ile Thr Ile Thr Trp Gln Lys Asp Gly Arg Pro Ile Pro Gly Ser
 625 630 635 640
 Leu Gly Val Thr Ile Asp Asn Ile Asp Phe Thr Ser Ser Leu Arg Ile
 645 650 655
 Ser Asn Leu Ser Leu Met His Asn Gly Asn Tyr Thr Cys Ile Ala Arg
 660 665 670
 Asn Glu Ala Ala Ala Val Glu His Gln Ser Gln Leu Ile Val Arg Val
 675 680 685
 Pro Pro Lys Phe Val Val Gln Pro Arg Asp Gln Asp Gly Ile Tyr Gly
 690 695 700
 Lys Ala Val Ile Leu Asn Cys Ser Ala Glu Gly Tyr Pro Val Pro Thr
 705 710 715 720
 Ile Val Trp Lys Phe Ser Lys Gly Ala Gly Val Pro Gln Phe Gln Pro
 725 730 735
 Ile Ala Leu Asn Gly Arg Ile Gln Val Leu Ser Asn Gly Ser Leu Leu
 740 745 750
 Ile Lys His Val Val Glu Glu Asp Ser Gly Tyr Tyr Leu Cys Lys Val
 755 760 765
 Ser Asn Asp Val Gly Ala Asp Val Ser Lys Ser Met Tyr Leu Thr Val
 770 775 780
 Lys Ile Pro Ala Met Ile Thr Ser Tyr Pro Asn Thr Thr Leu Ala Thr
 785 790 795 800

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Leu Gly Glu Ile Lys Asn Ile Thr Thr Thr Gln Pro Ser Leu Glu Leu
 1140 1145 1150
 Asp Gly Leu Glu Lys Tyr Thr Asn Tyr Ser Ile Gln Val Leu Ala Phe
 1155 1160 1165
 Thr Arg Ala Gly Asp Gly Val Arg Ser Glu Gln Ile Phe Thr Arg Thr
 1170 1175 1180
 Lys Glu Asp Val Pro Gly Pro Pro Ala Gly Val Lys Ala Ala Ala Ala
 1185 1190 1195 1200
 Ser Ala Ser Met Val Phe Val Ser Trp Leu Pro Pro Leu Lys Leu Asn
 1205 1210 1215
 Gly Ile Ile Arg Lys Tyr Thr Val Phe Cys Ser His Pro Tyr Pro Thr
 1220 1225 1230
 Val Ile Ser Glu Phe Glu Ala Ser Pro Asp Ser Phe Ser Tyr Arg Ile
 1235 1240 1245
 Pro Asn Leu Ser Arg Asn Arg Gln Tyr Ser Val Trp Val Val Ala Val
 1250 1255 1260
 Thr Ser Ala Gly Arg Gly Asn Ser Ser Glu Ile Ile Thr Val Glu Pro
 1265 1270 1275 1280
 Leu Ala Lys Ala Pro Ala Arg Ile Leu Thr Phe Ser Gly Thr Val Thr
 1285 1290 1295
 Thr Pro Trp Met Lys Asp Ile Val Leu Pro Cys Lys Ala Val Gly Asp
 1300 1305 1310
 Pro Ser Pro Ala Val Lys Trp Met Lys Asp Ser Asn Gly Thr Pro Ser
 1315 1320 1325
 Leu Val Thr Ile Asp Gly Arg Arg Ser Ile Phe Ser Asn Gly Ser Phe
 1330 1335 1340
 Ile Ile Arg Thr Val Lys Ala Glu Asp Ser Gly Tyr Tyr Ser Cys Ile
 1345 1350 1355 1360
 Ala Asn Asn Asn Trp Gly Ser Asp Glu Ile Ile Leu Asn Leu Gln Val
 1365 1370 1375
 Gln Val Pro Pro Asp Gln Pro Arg Leu Thr Val Ser Lys Thr Thr Ser
 1380 1385 1390
 Ser Ser Ile Thr Leu Ser Trp Leu Pro Gly Asp Asn Gly Gly Ser Ser
 1395 1400 1405
 Ile Arg Gly Tyr Ile Leu Gln Tyr Ser Glu Asp Asn Ser Glu Gln Trp
 1410 1415 1420
 Gly Ser Phe Pro Ile Ser Pro Ser Glu Arg Ser Tyr Arg Leu Glu Asn
 1425 1430 1435 1440
 Leu Lys Cys Gly Thr Trp Tyr Lys Phe Thr Leu Thr Ala Gln Asn Gly
 1445 1450 1455
 Val Gly Pro Gly Arg Ile Ser Glu Ile Ile Glu Ala Lys Thr Leu Gly
 1460 1465 1470

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